

32-13710: TIE1 Human

Format : The TIE1 solution (0.5mg/ml) contains 20mM Tris-HCl (pH 8.0), 0.1M NaCl and 50% glycerol.

Alternative Name : Tyrosine-protein kinase receptor Tie-1, TIE1, TIE, JTK14, LMPHM11.

Description

Source:HEK293 Cells.

Physical Appearance:Sterile Filtered colorless solution.

Biological Activity:null

TIE1 is an angiopoietin receptor which takes part in hematopoiesis, angiogenesis and vasculogenesis. TIE1 is expressed primarily on endothelial and hematopoietic progenitor cells. TIE1 is expressed in immature hematopoietic Recombinant Human TIE1 protein cells and platelets. TIE1 upregulates the cell adhesion molecules (CAMs) VCAM-1, ICAM-1 and E-selectin through a p38-dependent mechanism. TIE1 has a proinflammatory effect and takes part in the endothelial inflammatory diseases such as atherosclerosis.

TIE1 Human Recombinant produced in HEK293 Cells is a single, glycosylated polypeptide chain containing 977 amino acids (22-759 a.a) and having a molecular mass of 106.8kDa. TIE1 is fused to a 239 amino acid hlgG-His-Tag at C-terminus and is purified by proprietary chromatographic techniques.

Product Info

Amount : 20 µg / 5 µg

Purification : Greater than 90.0% as determined by SDS-PAGE.

Storage condition : Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA). Avoid multiple freeze-thaw cycles.

Amino Acid : AVDLTLLANL RLTDPRFFL TCVSGEAGAG RGSDAWGPPL LLEKDDRIVR TPPGPPPLRLA RNGSHQVTLR
GFSKPSDLVG VFCVGGAGA RRTRVIYVHN SPGAHLLPK VTHTVNGDGT AVLSARVHKE KQTDVIWKS
GSYFYTLDWH EAQDGRFLLQ LPNVQPPSSG IYSATYLEAS PLGSAFFRLI VRGCGAGRWG PGCTKECPGC
LHGGVCHDHD GECVCPGFT GTRCEQACRE GRFGQSCQEQ CPGISGCRGL TFCLPDYGC
SCGSGWRGSQ CQEACAPGHF GADCRLQCQC QNGGTCDRFS GCVCPSGWHG VHCEKSDRIP
QILNMASELE FNLETMPRIN CAAAGNPPPV RGSIELRKPDT GTVLLSTKAI VEPEKTTAEF EVPRLLVADS
GFWECRVSTS GGQDSRRFKV NVKVPVPLA APRLLTKQSR QLVVSPVLSF SGDGPSTVR LHYPQDSTM
DWSTIVDPS ENVTLMNLRP KTGYSVRVQL SRPGEAGEGA WGPPTLMTTD CPEPLLQVWL
EGWHVEGTDR LRVSWSLPLV PGPLVGDGFL LRLWDGTRGQ ERRENVSSPQ ARTALLTGLT
PGTHYQLDVQ LYHCTLLGPA SPPAHVLLPP SGPPAPRHLH AQALSDSEIQ LTKWHPALP GPISKYVVEV
QVAGGAGDPL WIDVDRPEET STIIRGLNAS TRYLFMRAS IQGLGDWSNT VEESTLGNGL QAEGPVQESR
AAEGLDQLE PKSCDKTHC PPCPAPELLG GPSVFLPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTPP VLDSGGSFFL YSKLTVDKSR
WQQGNVFSCS VMHEALHNHY TQKLSLSLSPG KHHHHHH